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<110> Human Genome Sciences, Inc.

<120> Albumin Fusion Proteins

<130> PF545PCT

<140> Unassigned

<141> 2001-04-12

<150> 60/229,358

<151> 2000-04-12

<150> 60/256,931

<151> 2000-12-21

<150> 60/199,384

<151> 2000-04-25

<160> 90

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> primer useful to clone human growth hormone cDNA

<400> 1

ccaagaatt cccttatcca ggc

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<220>
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with non-cohesive ends.

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gataaagatt cccaac

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with non-cohesive ends.

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<400> 5
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with non-cohesive ends.

<400> 6

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<222> 1)..(19)

<223> invertase leader sequence

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<222> 20)..(24)

<223> first 5 amino acids of mature human serum albumin

<400> 7

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fragments with non-cohesive ends.

<400> 8

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<210> 9

<211> 27

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<213> Artificial Sequence

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fragments with non-cohesive ends.

<400> 9
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<400> 12
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	
180 185 190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu	
195 200 205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro	
210 215 220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys	
225 230 235 240	
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp	
245 250 255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser	
260 265 270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His	
275 280 285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser	
290 295 300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala	
305 310 315 320	
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg	
325 330 335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr	
340 345 350	

tat	gaa	acc	act	cta	gag	aag	tgc	tgt	gcc	gct	gca	gat	cct	cat	gaa	1104
Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	
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Cys	Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	
	370					375					380					
cag	aat	tta	atc	aaa	caa	aac	tgt	gag	ctt	ttt	gag	cag	ctt	gga	gag	1200
Gln	Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu	
	385				390					395				400		
tac	aaa	ttc	cag	aat	gcg	cta	tta	gtt	cgt	tac	acc	aag	aaa	gta	ccc	1248
Tyr	Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	
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caa	gtg	tca	act	cca	act	ctt	gta	gag	gtc	tca	aga	aac	cta	gga	aaa	1296
Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	
			420					425					430			
gtg	ggc	agc	aaa	tgt	tgt	aaa	cat	cct	gaa	gca	aaa	aga	atg	ccc	tgt	1344
Val	Gly	Ser	Lys	Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	
		435					440					445				
gca	gaa	gac	tat	cta	tcc	gtg	gtc	ctg	aac	cag	tta	tgt	gtg	ttg	cat	1392
Ala	Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	
		450				455					460					
gag	aaa	acg	cca	gta	agt	gac	aga	gtc	aca	aaa	tgc	tgc	aca	gag	tcc	1440
Glu	Lys	Thr	Pro	Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	
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ttg	gtg	aac	agg	cga	cca	tgc	ttt	tca	gct	ctg	gaa	gtc	gat	gaa	aca	1488
Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	
				485					490					495		
tac	gtt	ccc	aaa	gag	ttt	aat	gct	gaa	aca	ttc	acc	ttc	cat	gca	gat	1536
Tyr	Val	Pro	Lys	Glu	Phe	Asn	Ala	Glu	Thr	Phe	Thr	Phe	His	Ala	Asp	
			500					505					510			
ata	tgc	aca	ctt	tct	gag	aag	gag	aga	caa	atc	aag	aaa	caa	act	gca	1584
Ile	Cys	Thr	Leu	Ser	Glu	Lys	Glu	Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala	
		515					520					525				
ctt	gtt	gag	ctt	gtg	aaa	cac	aag	ccc	aag	gca	aca	aaa	gag	caa	ctg	1632
Leu	Val	Glu	Leu	Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu	
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aaa	gct	gtt	atg	gat	gat	ttc	gca	gct	ttt	gta	gag	aag	tgc	tgc	aag	1680
Lys	Ala	Val	Met	Asp	Asp	Phe	Ala	Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys	

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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val							
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gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag	1782
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<210> 18
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 <212> PRT
 <213> Homo Sapiens

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu	
35 40 45	
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys	
50 55 60	
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu	
65 70 75 80	
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro	
85 90 95	
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu	
100 105 110	
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His	
115 120 125	
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
130 135 140	
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	

180					185					190					
Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu
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Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro
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Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys
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Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp
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Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His
		275					280					285			
Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser
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Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala
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Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg
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Arg	His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr
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Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu
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Cys	Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro
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Gln	Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu
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Tyr	Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro
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Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys
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Ala	Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His

450					455					460					
Glu	Lys	Thr	Pro	Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser
465					470					475					480
Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr
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Tyr	Val	Pro	Lys	Glu	Phe	Asn	Ala	Glu	Thr	Phe	Thr	Phe	His	Ala	Asp
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Ile	Cys	Thr	Leu	Ser	Glu	Lys	Glu	Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala
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Leu	Val	Glu	Leu	Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu
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Lys	Ala	Val	Met	Asp	Asp	Phe	Ala	Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys
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Ala	Asp	Asp	Lys	Glu	Thr	Cys	Phe	Ala	Glu	Glu	Gly	Lys	Lys	Leu	Val
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 <223> primer used to generate XhoI and ClaI
 site in pPPC0006

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<210> 20
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 <223> primer used in generation XhoI and ClaI
 site in pPPC0006

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<223> primer used in generation XhoI and ClaI
site in pPPC0006

<400> 21
tacaaactta agagtccaat tagc 24

<210> 22
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<212> DNA
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<223> primer used in generation XhoI and ClaI
site in pPPC0006

<400> 22
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<210> 23
<211> 60
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<220>
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<223> Synthetic oligonucleotide used to alter restriction
sites in pPPC0007

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 sites in pPPC0007

 <400> 24
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 <220>
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 <223> forward primer useful for generation of albumin
 fusion protein in which the albumin moiety is N-terminal
 of the Therapeutic Protein

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 <222> (18)
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<212> DNA

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<221> primer_bind

<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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gcgcgcgttt aaacggccgg ccggcgcgcc ttattannnn nnnnnnnnnn n

51

<210> 27

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<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

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<222> (19)

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aggagcgtcg acaaaagann nnnnnnnnnn nnn

33

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<220>
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<223> reverse primer useful for generation of albumin
fusion protein in which the albumin moiety is c-terminal of
the Therapeutic Protein

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<223> n equals a,t,g, or c

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ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nn

52

<210> 29

<211> 24

<212> PRT

<213> Artificial Sequence

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<221> signal

<223> signal peptide of natural human serum albumin protein

<400> 29

Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg
20

<210> 30

<211> 114

<212> DNA

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<220>

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<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>

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<222> (5)..(10)

<223> BamHI restriction site

<220>

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<222> (11)..(16)

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<222> (17)..(27)

<223> Kozak sequence

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<220>
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<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
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<222> (75)..(81)
<223> XhoI restriction site

<220>
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<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcaggggatcc aagcttccgc caccatgaag tgggtaacct ttatttcctc tctttttctc 60

ttagctcgg cttactcgag ggggtgtgtt cgtcgagatg cacacaagag tgag          114

<210> 31
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<220>
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<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<222> (12)..(17)
<223> EcoRI restriction site

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<220>
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<222> (18)..(25)
<223> AscI restriction site

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<220>
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 <222> (18)..(43)
 <223> reverse complement of DNA sequence encoding last 9 amino acids

 <400> 31
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 <210> 32
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> forward primer useful for inserting Therapeutic
 protein into pC4:HSA vector

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<223> n equals a,t,g, or c

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ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn

46

<210> 33

<211> 55

<212> DNA

<213> Artificial Sequence

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<223> reverse primer useful for inserting Therapeutic protein into pC4:HSA vector

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 <210> 34
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> signal
 <223> Stanniocalcin signal peptide

 <400> 34
 Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
 1 5 10 15

 Ala

 <210> 35
 <211> 22
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> signal
 <223> Synthetic signal peptide

 <400> 35
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 1 5 10 15

 Trp Ala Pro Ala Arg Gly
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 <210> 36
 <211> 23
 <212> DNA
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 <220>
 <221> primer_bind
 <223> Degenerate VH forward primer useful for
 amplifying human VH domains

<400> 36
 caggtgcagc tgggtgcagtc tgg 23

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence

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 <223>Degenerate VH forward primer useful for
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<400> 37
 caggtcaact taaggagtc tgg 23

<210> 38
 <211> 23
 <212> DNA
 <213> Artificial Sequence

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<400> 38
 gaggtgcagc tgggtggagtc tgg 23

<210> 39
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 <212> DNA
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<220>
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<400> 39
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<210> 40
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 <212> DNA
 <213> Artificial Sequence

<220>

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<400> 40
 gaggtgcagc tgttcagtc tgc 23

<210> 41
 <211> 23
 <212> DNA
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<400> 41
 caggtacagc tgcagcagtc agg 23

<210> 42
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 <212> DNA
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<400> 42
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<210> 43
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<400> 43
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<210> 44
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 <212> DNA
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<400> 44
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<400> 45
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<210> 46
 <211> 23
 <212> DNA
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<220>
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 <223>Degenerate Vkappa forward primer useful for
 amplifying human VL domains

<400> 46
 gacatccaga tgacccagtc tcc 23

<210> 47
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 47
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<210> 48
 <211> 23
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<213> Artificial Sequence

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<221>primer_bind

<223>Degenerate Vkappa forward primer useful for
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<400> 48

gatattgtga tgactcagtc tcc

23

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

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<221>primer_bind

<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 49

gaaattgtgt tgacgcagtc tcc

23

<210> 50

<211> 23

<212> DNA

<213> Artificial Sequence

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<223>Degenerate Vkappa forward primer useful for
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<400> 50

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23

<210> 51

<211> 23

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<223>Degenerate Vkappa forward primer useful for
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<400> 51

gaaacgacac tcacgcagtc tcc

23

<210> 52

<211> 23

<212> DNA
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 <210> 53
 <211> 23
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 <400> 53
 cagtctgtgt tgacgcagcc gcc 23

 <210> 54
 <211> 23
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 <400> 54
 cagtctgccc tgactcagcc tgc 23

 <210> 55
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 <400> 55
 tcctatgtgc tgactcagcc acc 23

 <210> 56

<211> 23
 <212> DNA
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<220>
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 amplifying human VL domains

<400> 56
 tcttctgagc tgactcagga ccc 23

<210> 57
 <211> 23
 <212> DNA
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<220>
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 amplifying human VL domains

<400> 57
 cacgttatac tgactcaacc gcc 23

<210> 58
 <211> 23
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<400> 58
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<210> 59
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<400> 59
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<210> 60
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 <400> 60
 acgtttgatt tccaccttgg tccc 24

 <210> 61
 <211> 24
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 <220>
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 <400> 61
 acgtttgatc tccagcttgg tccc 24

 <210> 62
 <211> 24
 <212> DNA
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 <400> 62
 acgtttgata tccactttgg tccc 24

 <210> 63
 <211> 24
 <212> DNA
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 <400> 63
 acgtttgatc tccaccttgg tccc 24

<210> 64
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 <212> DNA
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 <400> 64
 acgtttaatc tccagtcgtg tccc 24

 <210> 65
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 amplifying human VL domains

 <400> 65
 cagtctgtgt tgacgcagcc gcc 23

 <210> 66
 <211> 23
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 <220>
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 <400> 66
 cagtctgccc tgactcagcc tgc 23

 <210> 67
 <211> 23
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 <400> 67

tcctatgtgc tgactcagcc acc 23

<210> 68

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate Jlambda reverse primer useful for
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<400> 68

tcttctgagc tgactcagga ccc 23

<210> 69

<211> 23

<212> DNA

<213> Artificial Sequence

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<223>Degenerate Jlambda reverse primer useful for
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<400> 69

cacgttatac tgactcaacc gcc 23

<210> 70

<211> 23

<212> DNA

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<223>Degenerate Jlambda reverse primer useful for
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<400> 70

caggctgtgc tcactcagcc gtc 23

<210> 71

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate Jlambda reverse primer useful for
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<400> 71
aattttatgc tgactcagcc cca

23

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221>turn
<223>Linker peptide that may be used to join VH
and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 73
<211> 23
<212> PRT
<213> Homo sapiens

<400> 73
Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala
1 5 10 15

Thr Cys Cys Ala Gly Gly Cys
20

<210> 74
<211> 429
<212> PRT
<213> Homo sapiens

<400> 74
Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu
1 5 10 15

Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser
20 25 30

Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu
35 40 45

Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val
50 55 60

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys
65 70 75 80

Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr

355 360 365
 Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe
 370 375 380
 Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro
 385 390 395 400
 Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr
 405 410 415
 His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg
 420 425

 <210> 75
 <211> 280
 <212> PRT
 <213> Homo sapiens

 <400> 75
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 1 5 10 15
 Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg
 20 25 30
 Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met
 35 40 45
 Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro
 50 55 60
 Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile
 65 70 75 80
 Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile
 85 90 95
 Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg
 100 105 110
 Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser
 115 120 125
 Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro
 130 135 140
 Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met
 145 150 155 160
 Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro

					165						170						175
Val	Trp	Gly	Ser	Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly		
			180					185					190				
Leu	Leu	Leu	Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro		
		195					200					205					
Ser	Lys	Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu		
	210					215					220						
Leu	Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu		
225					230					235					240		
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu	Gly		
				245					250					255			
Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser	Leu	Gly		
			260					265					270				
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		275					280										

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 <212> PRT
 <213> Homo sapiens

<400> 76

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			20					25					30				
His	Ala	Pro	Val	Pro	Gln	Ser	Ile	Cys	Pro	Arg	Tyr	Thr	Ser	Pro	Cys		
		35					40					45					
Ala	Pro	His	Asp	Cys	Gly	Ser	Gln	Thr	Val	Gln	Gly	Asn	Ser	Leu	Ser		
	50					55					60						
Leu	Phe	Tyr	Thr	Leu	Ser	His	Lys	Ala	Pro	Gln	Leu	Pro	His	Arg	Val		
65					70					75					80		
Pro	Ala	Pro	Leu	Phe	Cys	Lys	Tyr	Val	Lys	Arg	Lys	Lys	Cys	Lys	Arg		
				85					90						95		
Trp	Ser	Leu	Gly	Trp	Ser	Ser	Ser	Leu	Gln	Leu	Arg	Leu	Leu	Thr	Met		
			100					105					110				

<210> 77

<211> 346
 <212> PRT
 <213> Homo sapiens

<400> 77

Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln	Ala	Met	Ile	Trp	Thr	Ala
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Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala	Leu	Glu
			20					25					30		
Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser	Pro	Asn	Lys
		35					40					45			
Met	Lys	Thr	Val	Lys	Cys	Ala	Pro	Gly	Val	Asp	Val	Cys	Thr	Glu	Ala
	50					55					60				
Val	Gly	Ala	Val	Glu	Thr	Ile	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Arg
65					70					75					80
Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	Asp	Arg	Gly	Leu	Asp	Leu
				85					90					95	
His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	Gln	Cys	Ala	Gln	Asp	Arg
			100					105					110		
Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr	Ser	Arg	Ala	Leu	Asp	Pro	Ala	Gly
		115					120					125			
Asn	Glu	Ser	Ala	Tyr	Pro	Pro	Asn	Gly	Val	Glu	Cys	Tyr	Ser	Cys	Val
	130					135					140				
Gly	Leu	Ser	Arg	Glu	Ala	Cys	Gln	Gly	Thr	Ser	Pro	Pro	Val	Val	Ser
145					150					155					160
Cys	Tyr	Asn	Ala	Ser	Asp	His	Val	Tyr	Lys	Gly	Cys	Phe	Asp	Gly	Asn
				165					170					175	
Val	Thr	Leu	Thr	Ala	Ala	Asn	Val	Thr	Val	Ser	Leu	Pro	Val	Arg	Gly
			180					185					190		
Cys	Val	Gln	Asp	Glu	Phe	Cys	Thr	Arg	Asp	Gly	Val	Thr	Gly	Pro	Gly
		195					200					205			
Phe	Thr	Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	Ser	Arg	Cys	Asn	Ser	Asp
	210					215					220				
Leu	Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	Ile	Pro	Pro	Leu	Val	Arg
225					230					235					240
Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	Ser	Thr	Thr	Ser	Val	Thr

				245					250					255			
Thr	Ser	Thr	Ser	Ala	Pro	Val	Arg	Pro	Thr	Ser	Thr	Thr	Lys	Pro	Met		
			260					265					270				
Pro	Ala	Pro	Thr	Ser	Gln	Thr	Pro	Arg	Gln	Gly	Val	Glu	His	Glu	Ala		
		275					280					285					
Ser	Arg	Asp	Glu	Glu	Pro	Arg	Leu	Thr	Gly	Gly	Ala	Ala	Gly	His	Gln		
	290					295					300						
Asp	Arg	Ser	Asn	Ser	Gly	Gln	Tyr	Pro	Ala	Lys	Gly	Gly	Pro	Gln	Gln		
305					310					315					320		
Pro	His	Asn	Lys	Gly	Cys	Val	Ala	Pro	Thr	Ala	Gly	Leu	Ala	Ala	Leu		
				325					330					335			
Leu	Leu	Ala	Val	Ala	Ala	Gly	Val	Leu	Leu								
			340					345									
<210> 78																	
<211> 272																	
<212> PRT																	
<213> Homo sapiens																	
<400> 78																	
Met	Lys	Gly	Lys	Lys	Gly	Ile	Val	Ala	Ala	Ser	Gly	Ser	Glu	Thr	Glu		
1				5					10					15			
Asp	Glu	Asp	Ser	Met	Asp	Ile	Pro	Leu	Asp	Leu	Ser	Ser	Ser	Ala	Gly		
			20					25					30				
Ser	Gly	Lys	Arg	Arg	Arg	Arg	Gly	Asn	Leu	Pro	Lys	Glu	Ser	Val	Gln		
		35					40					45					
Ile	Leu	Arg	Asp	Trp	Leu	Tyr	Glu	His	Arg	Tyr	Asn	Ala	Tyr	Pro	Ser		
	50					55					60						
Glu	Gln	Glu	Lys	Ala	Leu	Leu	Ser	Gln	Gln	Thr	His	Leu	Ser	Thr	Leu		
65					70					75					80		
Gln	Val	Cys	Asn	Trp	Phe	Ile	Asn	Ala	Arg	Arg	Arg	Leu	Leu	Pro	Asp		
				85					90					95			
Met	Leu	Arg	Lys	Asp	Gly	Lys	Asp	Pro	Asn	Gln	Phe	Thr	Ile	Ser	Arg		
			100					105					110				
Arg	Gly	Ala	Lys	Ile	Ser	Glu	Thr	Ser	Ser	Val	Glu	Ser	Val	Met	Gly		
		115					120					125					
Ile	Lys	Asn	Phe	Met	Pro	Ala	Leu	Glu	Glu	Thr	Pro	Phe	His	Ser	Cys		

130		135		140
Thr 145	Ala Gly Pro	Asn Pro 150	Thr Leu Gly Arg Pro 155	Leu Ser Pro Lys Pro 160
Ser	Ser Pro Gly	Ser Val 165	Leu Ala Arg Pro 170	Ser Val Ile Cys His Thr 175
Thr	Val Thr	Ala Leu Lys Asp Val 180	Phe Ser Leu Cys Gln Ser Val 185	
Gly	Val Gly	Gln Asn Thr Asp Ile 195	Gln Gln Ile Ala Ala Lys Asn Phe 200	
Thr	Asp Thr	Ser Leu Met Tyr Pro Glu Asp Thr 210	Cys Lys Ser Gly Pro 215	
Ser 225	Thr Asn Thr	Gln Ser Gly Leu Phe Asn Thr 230	Pro Pro Pro Thr Pro 235	
Pro	Asp Leu Asn	Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val 245		
Ala	Leu Lys Arg	Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala 260		

<210> 79
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 79
 Met 1 Leu Thr Val Ala 5 Leu Leu Ala Leu 10 Leu Cys Ala Ser Ala 15 Ser Gly

Asn	Ala Ile	Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly
	20	25 30
Gly	Gly Gly	Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro
	35	40 45
Ile	Thr Ala	Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu
	50	55 60
Gln	Val Arg Tyr	Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn
	65	70 75 80
Gly	Asp Leu	Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln
	85	90 95
Val	Ser Gly	Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr

100	105	110
Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe		
115	120	125
Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly		
130	135	140
Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr		
145	150	155
Pro Thr Ser Cys Ser Arg Cys		
165		

<210> 80
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (22)
 <223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala
1 5 10 15
His Ser Gly Arg Ala Xaa
20

<210> 81
 <211> 733
 <212> DNA
 <213> Homo sapiens

<400> 81

gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg	60
aattcgaggg tgcaccgtca gtcttcctct tcccccaaa acccaaggac accctcatga	120
tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg	180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg	240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact	300
ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca acccccatcg	360

agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc	420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct	480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga	540
ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctcaccgtgg	600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc	660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc	720
gactctagag gat	733

<210> 82
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_structure
 <223> membrane proximal motif of class 1 cytokine receptors

<220>
 <221> misc_feature
 <222> (3)
 <223> Xaa equals any

<400> 82
 Trp Ser Xaa Trp Ser
 1 5

<210> 83
 <211> 86
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> forward primer useful for generation of a synthetic gamma
 activation site (GAS) containing promoter element

<400> 83	
ggcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc	60
cccgaaatat ctgccatctc aattag	86

<210> 84
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> reverse primer useful for generation of a synthetic gamma
 activation site (GAS) containing promoter element

 <400> 84
 gcggcaagct ttttgcaaag cctaggc 27

 <210> 85
 <211> 271
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <223> Synthetic GAS-SV40 promoter sequence

 <400> 85
 ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
 aaatatctgc catctcaatt agtcagcaac catagtccccg cccctaactc cgcccatccc 120
 gccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
 ttttgagggc ctaggctttt gcaaaaagct t 271

 <210> 86
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer useful for generation of a EGR/SEAP reporter construct

 <400> 86
 gcgctcgagg gatgacagcg atagaacccc gg 32

 <210> 87
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> primer useful for generation of a EGR/SEAP reporter construct

 <400> 87
 gcgaagcttc gcgactcccc ggatccgcct c 31

 <210> 88
 <211> 12
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_binding
 <223> NF-KB binding site

 <400> 88
 ggggactttc cc 12

 <210> 89
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> forward primer useful for generation of a vector containing the
 NF-KB promoter element

 <400> 89
 gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60
 ccatctcaat tag 73

 <210> 90
 <211> 256
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <223> Synthetic NF-KB/SV40 promoter

 <400> 90
 ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60
 caattagtca gcaaccatag tcccgccct aactccgccc atcccgcccc taactccgcc 120
 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg	240
cttttgcaaa aagctt	256